

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY TO CYTOKININ
RECEPTOR

<130> P152622

<160> 22

<170> PatentIn Ver. 2.1

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<211> 3531

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (1)..(3531)

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aag tcg tcg agc agt gac aag aaa tgg cta aag aag cct ctc ttc ttc				96
Lys Ser Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe				
20		25	30	
ctg att ttg tgt ggc tct ttg gta att gtt ttg gtt atg ttc tta cgg				144
Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg				
35		40	45	
tta ggt aga agt cag aag gag gag aca gat tct tgt aat gga gaa gag				192
Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu				
50		55	60	
aaa gtg ttg tat aga cat caa aat gtc aca aga agt gag att cat gat				240
Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp				
65	70	75	80	
ttg gtc tct ttg ttc tct gat tca gat cag gta aca tcc ttt gaa tgt				288
Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys				
85		90	95	

tgg tgg tgt cta atc ctt ggt gtg tta gtg tgc cat aag att tat gta 576

Trp Trp Cys Leu Ile Leu Gly Val Leu Val Cys His Lys Ile Tyr Val
180 185 190

tct cat tct aaa gca cga ggt gag agg aaa gag aaa gta cat ctg caa 624

Ser His Ser Lys Ala Arg Gly Glu Arg Lys Glu Lys Val His Leu Gln
195 200 205

gag gct tta gct cca aag aag cag caa caa cgt gct cag act tct tct 672

Glu Ala Leu Ala Pro Lys Lys Gln Gln Gln Arg Ala Gln Thr Ser Ser
210 215 220

aga ggg gct gga aga tgg agg aag aat atc ctt ctc ctt ggt att tta 720

Arg Gly Ala Gly Arg Trp Arg Lys Asn Ile Leu Leu Leu Gly Ile Leu
225 230 235 240

gga gga gtt tcc ttc tct gtt tgg tgg ttt tgg gac act aat gag gag 768

Gly Gly Val Ser Phe Ser Val Trp Trp Phe Trp Asp Thr Asn Glu Glu
245 250 255

atc ata atg aaa agg agg gag act ttg gca aac atg tgt gac gaa cga 816

Ser Glu Arg Glu Lys Phe Glu Lys Glu His Gly Trp Ala Ile Lys Lys
340 345 350

atg gaa act gag gac cag aca gtt gta caa gat tgt gtt cct gaa aac 1104

Met Glu Thr Glu Asp Gln Thr Val Val Gln Asp Cys Val Pro Glu Asn
355 360 365

ttt gat ccc gca ccg att caa gac gaa tac gcg cca gtt ata ttt gct 1152

Phe Asp Pro Ala Pro Ile Gln Asp Glu Tyr Ala Pro Val Ile Phe Ala
370 375 380

caa gaa act gtt tcc cat att gta tcg gtc gac atg atg tct gga gaa 1200

Gln Glu Thr Val Ser His Ile Val Ser Val Asp Met Met Ser Gly Glu
385 390 395 400

gaa gac cgt gaa aac atc tta cgg gca agg gca tca gga aaa gga gtg 1248

Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Ala Ser Gly Lys Gly Val
405 410 415

tta aca tct cca ttt aag ctt ctt aag tca aat cat ctt ggt gtt gtg 1296

Leu Thr Ser Pro Phe Lys Leu Leu Lys Ser Asn His Leu Gly Val Val

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ttg acc ttt gct gtc tat gac acg agc cta ccg cct gat gct aca gaa 1344

Leu Thr Phe Ala Val Tyr Asp Thr Ser Leu Pro Pro Asp Ala Thr Glu

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445

gaa cag cgt gtt gaa gca act att ggg tac ctt ggt gca tca tat gat 1392

Glu Gln Arg Val Glu Ala Thr Ile Gly Tyr Leu Gly Ala Ser Tyr Asp

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atg cca tcg ctg gtg gag aaa ctt ctt cac caa ctt gcc agc aaa cag 1440

Met Pro Ser Leu Val Glu Lys Leu Leu His Gln Leu Ala Ser Lys Gln

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aca att gct gtg gat gtt tac gac aca act aac act tca ggt cta ata 1488

Thr Ile Ala Val Asp Val Tyr Asp Thr Thr Asn Thr Ser Gly Leu Ile

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aaa atg tat ggc tca gaa att ggg gat ata agt gag cag cat ata agt 1536

Lys Met Tyr Gly Ser Glu Ile Gly Asp Ile Ser Glu Gln His Ile Ser

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agc ctt gat ttt ggt gat cca tca agg aac cat gag atg cat tgc agg 1584

Ser Leu Asp Phe Gly Asp Pro Ser Arg Asn His Glu Met His Cys Arg

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ttt aag cat aaa ctt ccc att ccc tgg aca gcg ata aca ccg tcg atc 1632

Phe Lys His Lys Leu Pro Ile Pro Trp Thr Ala Ile Thr Pro Ser Ile

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tta gtt ctg gtt att act ttt ctt gtt ggt tat att tta tat gaa gcc 1680

Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala

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atc aac cga att gcg aca gtt gaa gag gat tgt cag aag atg agg gaa 1728

Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu

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ctc aaa gct cgt gct gag gcc gct gac att gca aag tca cag ttc cta 1776

Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu

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gca act gtt tct cat gag ata cgg act ccg atg aat gga gtt tta gga 1824

Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly

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atg ctg aaa atg ctg atg gac acc gat ctt gat gcg aag cag atg gac 1872

Met Leu Lys Met Leu Met Asp Thr Asp Leu Asp Ala Lys Gln Met Asp

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tat gcg caa act gct cat ggc agt ggg aag gat ctt aca tca cta ata 1920

Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile

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aat gag gtt ctt gat cag gca aag att gaa tcc gga agg ctc gag ctt 1968

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Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser

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Gly Cys Ser Glu Ser Gly Glu Thr Val Ser Gly Phe Pro Ala Val Asn

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Ala Trp Gly Ser Trp Lys Asn Phe Lys Thr Cys Tyr Ser Thr Glu Ser

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Gln Asn Ser Asp Gln Ile Lys Leu Leu Val Thr Val Glu Asp Thr Gly

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gtt ggc ata cct gtg gat gca caa ggc cga atc ttc aca cct ttt atg 2448

Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met

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Gln Ala Asp Ser Ser Thr Ser Arg Thr Tyr Gly Gly Thr Gly Ile Gly

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Leu Ser Ile Ser Lys Arg Leu Val Glu Leu Met Gln Gly Glu Met Gly

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Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val

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ttc ggg aaa gca gaa aca aat acg tcg att act aag ctg gaa cga ttc 2640

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gat cta gct att cag gag ttt aca gga ttg aga gca tta gtt att gat 2688

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Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys

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tgt atc agc aaa tta gaa aat ttg gct atg att cta ata gac aaa gac 2832

Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp

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gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga 2880

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gat gat aat ctt gtg aac aga cga gtt gca gaa ggt gca ctt aag aaa 3168

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tat gga gct att gtt aca tgc gtt gag agt ggc aaa gct gca ttg gca 3216

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atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag 3264

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Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu

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gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg 3504

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25

30

Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg

35

40

45

Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu

50

55

60

Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp

65

70

75

80

Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys

85

90

95

His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys

100

105

110

Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp

115

120

125

Asn	Leu	Gly	Leu	Gly	His	Ser	Ile	Ser	Ser	Thr	Ser	Cys	Met	Cys	Gly
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His	Glu	Glu	Gly	Leu	Glu	Gln	Gly	Leu	Ser	Ser	Tyr	Leu	Arg	Asn	Ala
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Trp	Trp	Cys	Leu	Ile	Leu	Gly	Val	Leu	Val	Cys	His	Lys	Ile	Tyr	Val
		180						185					190		
Ser	His	Ser	Lys	Ala	Arg	Gly	Glu	Arg	Lys	Glu	Lys	Val	His	Leu	Gln
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Gly	Gly	Val	Ser	Phe	Ser	Val	Trp	Trp	Phe	Trp	Asp	Thr	Asn	Glu	Glu
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Ile	Ile	Met	Lys	Arg	Arg	Glu	Thr	Leu	Ala	Asn	Met	Cys	Asp	Glu	Arg
		260						265					270		
Ala	Arg	Val	Leu	Gln	Asp	Gln	Phe	Asn	Val	Ser	Leu	Asn	His	Val	His
		275					280						285		
Ala	Leu	Ser	Ile	Leu	Val	Ser	Thr	Phe	His	His	Gly	Lys	Ile	Pro	Ser
	290						295					300			
Ala	Ile	Asp	Gln	Arg	Thr	Phe	Glu	Glu	Tyr	Thr	Glu	Arg	Thr	Asn	Phe
305				310						315					320
Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala	Leu	Lys	Val	Pro	His
				325						330				335	

Ser	Glu	Arg	Glu	Lys	Phe	Glu	Lys	Glu	His	Gly	Trp	Ala	Ile	Lys	Lys
				340				345						350	
Met	Glu	Thr	Glu	Asp	Gln	Thr	Val	Val	Gln	Asp	Cys	Val	Pro	Glu	Asn
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Phe	Asp	Pro	Ala	Pro	Ile	Gln	Asp	Glu	Tyr	Ala	Pro	Val	Ile	Phe	Ala
				370				375						380	
Gln	Glu	Thr	Val	Ser	His	Ile	Val	Ser	Val	Asp	Met	Met	Ser	Gly	Glu
				385				390						395	400
Glu	Asp	Arg	Glu	Asn	Ile	Leu	Arg	Ala	Arg	Ala	Ser	Gly	Lys	Gly	Val
				405				410						415	
Leu	Thr	Ser	Pro	Phe	Lys	Leu	Leu	Lys	Ser	Asn	His	Leu	Gly	Val	Val
				420				425						430	
Leu	Thr	Phe	Ala	Val	Tyr	Asp	Thr	Ser	Leu	Pro	Pro	Asp	Ala	Thr	Glu
				435				440						445	
Glu	Gln	Arg	Val	Glu	Ala	Thr	Ile	Gly	Tyr	Leu	Gly	Ala	Ser	Tyr	Asp
				450				455						460	
Met	Pro	Ser	Leu	Val	Glu	Lys	Leu	Leu	His	Gln	Leu	Ala	Ser	Lys	Gln
				465				470						475	480
Thr	Ile	Ala	Val	Asp	Val	Tyr	Asp	Thr	Thr	Asn	Thr	Ser	Gly	Leu	Ile
				485				490						495	
Lys	Met	Tyr	Gly	Ser	Glu	Ile	Gly	Asp	Ile	Ser	Glu	Gln	His	Ile	Ser
				500				505						510	
Ser	Leu	Asp	Phe	Gly	Asp	Pro	Ser	Arg	Asn	His	Glu	Met	His	Cys	Arg
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Phe	Lys	His	Lys	Leu	Pro	Ile	Pro	Trp	Thr	Ala	Ile	Thr	Pro	Ser	Ile
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Leu Val Leu Val Ile Thr Phe Leu Val Gly Tyr Ile Leu Tyr Glu Ala
 545 550 555 560
 Ile Asn Arg Ile Ala Thr Val Glu Glu Asp Cys Gln Lys Met Arg Glu
 565 570 575
 Leu Lys Ala Arg Ala Glu Ala Ala Asp Ile Ala Lys Ser Gln Phe Leu
 580 585 590
 Ala Thr Val Ser His Glu Ile Arg Thr Pro Met Asn Gly Val Leu Gly
 595 600 605
 Met Leu Lys Met Leu Met Asp Thr Asp Leu Asp Ala Lys Gln Met Asp
 610 615 620
 Tyr Ala Gln Thr Ala His Gly Ser Gly Lys Asp Leu Thr Ser Leu Ile
 625 630 635 640
 Asn Glu Val Leu Asp Gln Ala Lys Ile Glu Ser Gly Arg Leu Glu Leu
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 Glu Asn Val Pro Phe Asp Met Arg Phe Ile Leu Asp Asn Val Ser Ser
 660 665 670
 Leu Leu Ser Gly Lys Ala Asn Glu Lys Gly Ile Glu Leu Ala Val Tyr
 675 680 685
 Val Ser Ser Gln Val Pro Asp Val Val Val Gly Asp Pro Ser Arg Phe
 690 695 700
 Arg Gln Ile Ile Thr Asn Leu Val Gly Asn Ser Ile Lys Phe Thr Gln
 705 710 715 720
 Glu Arg Gly His Ile Phe Ile Ser Val His Leu Ala Asp Glu Val Lys
 725 730 735
 Glu Pro Leu Thr Ile Glu Asp Ala Val Leu Lys Gln Arg Leu Ala Leu
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Gly Cys Ser Glu Ser Gly Glu Thr Val Ser Gly Phe Pro Ala Val Asn			
755	760	765	
Ala Trp Gly Ser Trp Lys Asn Phe Lys Thr Cys Tyr Ser Thr Glu Ser			
770	775	780	
Gln Asn Ser Asp Gln Ile Lys Leu Leu Val Thr Val Glu Asp Thr Gly			
785	790	795	800
Val Gly Ile Pro Val Asp Ala Gln Gly Arg Ile Phe Thr Pro Phe Met			
	805	810	815
Gln Ala Asp Ser Ser Thr Ser Arg Thr Tyr Gly Gly Thr Gly Ile Gly			
	820	825	830
Leu Ser Ile Ser Lys Arg Leu Val Glu Leu Met Gln Gly Glu Met Gly			
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Phe Val Ser Glu Pro Gly Ile Gly Ser Thr Phe Ser Phe Thr Gly Val			
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Phe Gly Lys Ala Glu Thr Asn Thr Ser Ile Thr Lys Leu Glu Arg Phe			
865	870	875	880
Asp Leu Ala Ile Gln Glu Phe Thr Gly Leu Arg Ala Leu Val Ile Asp			
	885	890	895
Asn Arg Asn Ile Arg Ala Glu Val Thr Arg Tyr Glu Leu Arg Arg Leu			
	900	905	910
Gly Ile Ser Ala Asp Ile Val Ser Ser Leu Arg Met Ala Cys Thr Cys			
	915	920	925
Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp			
	930	935	940
Ala Trp Asn Lys Glu Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg			
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Val Ala Arg Phe Phe Glu Pro Cys

1170

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atc gag gac aag tct ggt ctt tta gtt ggc tct gtc ggt gat ctt gag 144

Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu

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aag act aag atg act acg ttg aag aag aag aac aag atg tgg ttc tgg 192

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp

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aat aag atc tct agc agc gga ctc aag atc ccg agt ttc tct tat cag 240

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln

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ttt ctt ggc tct gtt aaa ttc aac aag gcg tgg tgg agg aag ctt gtg 288

Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val

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90

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gtg gtt tgg gtt gtc ttc tgg gtc ttg gtc tct att tgg acg ttt tgg 336

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp

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tac ttt agc tcg caa gct atg gag aag agg aaa gag acg cta gct agt 384

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser

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Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

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atg aat cat gtt caa gcc atg tct atc ttg atc tca acc ttc cac cat 480

Met Asn His Val Gln Ala Met Ser Ile Leu Ile Ser Thr Phe His His

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Gly Lys Ile Pro Ser Ala Ile Asp Gln Arg Thr Phe Ser Glu Tyr Thr

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gat aga act tcc ttt gag agg cct ctt act agc ggg gta gct tat gct 576

Asp Arg Thr Ser Phe Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala

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185

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atg agg gtg ctc cat tca gag agg gaa gag ttc gag agg caa caa ggt 624

Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly

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Trp Thr Ile Arg Lys Met Tyr Ser Leu Glu Gln Asn Pro Val His Lys

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Tyr Ala Pro Val Ile Phe Ala Gln Asp Thr Val Ser His Val Val Ser

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ctc gat atg ctg tct ggg aaa gaa gat cgt gaa aac gtt ttg cgg gcc 816

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260

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Arg Ser Ser Gly Lys Gly Val Leu Thr Ala Pro Phe Pro Leu Ile Lys

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Leu Pro Ser Asn Ala Thr Pro Lys Glu Arg Ile Glu Ala Thr Asn Gly
305 310 315 320

tat ctc ggg gga gtg ttt gac att gag tcc ctg gta gaa aac ttg ctt 1008

Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu
325 330 335

caa cag ctg gct agc aag caa acg att ctt gtc aat gtg tac gat atc 1056

Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile
340 345 350

acc aat cac tct caa ccg att agc atg tat ggt aca aat gtg tcg gct 1104

Thr Asn His Ser Gln Pro Ile Ser Met Tyr Gly Thr Asn Val Ser Ala
355 360 365

gat ggg ttg gaa cgt gtt agt cca cta atc ttt ggc gat cca ttg aga 1152

Asp Gly Leu Glu Arg Val Ser Pro Leu Ile Phe Gly Asp Pro Leu Arg
370 375 380

aag cat gag atg cgt tgc aga ttt aag cag aaa cca cca tgg cca gtg 1200

Lys His Glu Met Arg Cys Arg Phe Lys Gln Lys Pro Pro Trp Pro Val
385 390 395 400

cta tca atg gtg aca tca ttc ggt atc ctt gtg att gcg tta ctt gtt 1248

Leu Ser Met Val Thr Ser Phe Gly Ile Leu Val Ile Ala Leu Leu Val
405 410 415

gca cat ata atc cac gca acc gtt agt cga ata cac aaa gtt gaa gaa 1296

Ala His Ile Ile His Ala Thr Val Ser Arg Ile His Lys Val Glu Glu
420 425 430

gat tgt gat aaa atg aag cag ctc aag aaa aag gct gaa gca gca gat 1344

Asp Cys Asp Lys Met Lys Gln Leu Lys Lys Lys Ala Glu Ala Ala Asp
435 440 445

gtt gca aag tca cag ttc ctt gcc act gtt tca cat gaa atc aga act 1392

Val Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr

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cca atg aat ggt gtt cta gga atg ttg cat atg ctt atg gac aca gag 1440

Pro Met Asn Gly Val Leu Gly Met Leu His Met Leu Met Asp Thr Glu

465

470

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tta gat gtt acg caa cag gat tat gtt agg acc gca cag gca agt gga 1488

Leu Asp Val Thr Gln Gln Asp Tyr Val Arg Thr Ala Gln Ala Ser Gly

485

490

495

aaa gct tta gtc tcg cta ata aat gag gtt ttg gac caa gca aag att 1536

Lys Ala Leu Val Ser Leu Ile Asn Glu Val Leu Asp Gln Ala Lys Ile

500

505

510

gaa tct gga aag ctt gaa ctt gag gag gtg cgg ttt gat ttg aga gga 1584

Glu Ser Gly Lys Leu Glu Leu Glu Glu Val Arg Phe Asp Leu Arg Gly

515

520

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ata tta gat gat gtc ctg tca ctc ttc tct agc aag tcc caa caa aag 1632

Ile Leu Asp Asp Val Leu Ser Leu Phe Ser Ser Lys Ser Gln Gln Lys

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ggg gtg gag ttg gca gta tac ata tct gat cgt gtt cca gat atg tta 1680

Gly Val Glu Leu Ala Val Tyr Ile Ser Asp Arg Val Pro Asp Met Leu

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555

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Ile Gly Asp Pro Gly Arg Phe Arg Gln Ile Leu Thr Asn Leu Met Gly

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aat tcc att aag ttc act gag aaa gga cac atc ttt gta act gtt cat 1776

Asn Ser Ile Lys Phe Thr Glu Lys Gly His Ile Phe Val Thr Val His

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ttg gtg gat gag cta ttt gaa tct atc gat gga gag aca gca tca tct 1824

Leu Val Asp Glu Leu Phe Glu Ser Ile Asp Gly Glu Thr Ala Ser Ser

595

600

605

ccg gaa agt aca ctg agt ggg ctt cca gtt gca gac cgg cag agg agc 1872

Pro Glu Ser Thr Leu Ser Gly Leu Pro Val Ala Asp Arg Gln Arg Ser

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615

620

tgg gaa aac ttt aaa gct ttc agc tcc aac ggg cat cgg agc ttt gaa 1920

Trp Glu Asn Phe Lys Ala Phe Ser Ser Asn Gly His Arg Ser Phe Glu

625

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635

640

cca tct ccc cct gat ata aac cta atc gtc tca gtt gag gat act ggc 1968

Pro Ser Pro Pro Asp Ile Asn Leu Ile Val Ser Val Glu Asp Thr Gly

645

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655

gta ggg atc cct gta gaa gcg cag tcc cgt att ttt acg cct ttc atg 2016

Val Gly Ile Pro Val Glu Ala Gln Ser Arg Ile Phe Thr Pro Phe Met

660

665

670

caa gtc gga cca tcc ata tcc agg acg cat gga ggc aca gga att gga 2064

Gln Val Gly Pro Ser Ile Ser Arg Thr His Gly Gly Thr Gly Ile Gly

675

680

685

ctt agc ata agc aaa tgt cta gtt gga ctg atg aag gga gaa att gga 2112

Leu Ser Ile Ser Lys Cys Leu Val Gly Leu Met Lys Gly Glu Ile Gly

690

695

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ttc tgc agt act ccc aag gtt ggg tcc aca ttc aca ttt act gct gta 2160

Phe Ser Ser Thr Pro Lys Val Gly Ser Thr Phe Thr Phe Thr Ala Val
705 710 715 720

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Phe Ser Asn Gly Met Gln Pro Ala Glu Arg Lys Asn Asp Asn Asn Gln
725 730 735

ccc ata ttc tgc gaa ttc cgg ggc atg aaa gct gtg gtt gtg gac cat 2256

Pro Ile Phe Ser Glu Phe Arg Gly Met Lys Ala Val Val Val Asp His
740 745 750

agg cct gca agg gca aaa gtc tgc tgg tac cat ttt cag cgt ctt gga 2304

Arg Pro Ala Arg Ala Lys Val Ser Trp Tyr His Phe Gln Arg Leu Gly
755 760 765

att cga gtc gaa gta gtt cca cgt gtt gaa cag gct cta cat tat ctg 2352

Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu
770 775 780

aag att ggt act acc act gtg aat atg ata ctc ata gag caa gaa ata 2400

Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile
785 790 795 800

tgg aat agg gaa gca gat gat ttc att aaa aag cta cag aaa gac cct 2448

Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro
805 810 815

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Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser
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tca ata tca gag gct tta tgc acc ggt ata gat cct cca ata gtg ata 2544

Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile
835 840 845

gtg aaa cca ttg agg gcg agt atg cta gca gca act ttg cag agg gga 2592

Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly
850 855 860

ttg ggt att gga atc aga gaa cca cct caa cac aag gga cct cct gct 2640

Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala

865

870

875

880

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Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp

885

890

895

gat aac aac gta aac ctc aga gtg gca gcg gga gct ctg aaa aag tac 2736

Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr

900

905

910

gga gct gat gtg gtc tgc gct gag agt ggg ata aag gca atc tca ttg 2784

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915

920

925

ctt aag cca cct cac gag ttt gat gct tgc ttc atg gac att cag atg 2832

Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met

930

935

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cca gaa atg gat gga ttt gaa gct aca agg aga ata cga gat atg gaa 2880

Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu
 945 950 955 960

gag gag atg aac aag aga ata aag aat ggg gag gct tgg ata gta gag 2928

Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu
 965 970 975

aac ggt aac aaa aca agc tgg cat ctt ccg gta tta gca atg acg gca 2976

Asn Gly Asn Lys Thr Ser Trp His Leu Pro Val Leu Ala Met Thr Ala
 980 985 990

gat gtg atc caa gca acg cat gag gaa tgt ctg aag tgt gga atg gat 3024

Asp Val Ile Gln Ala Thr His Glu Glu Cys Leu Lys Cys Gly Met Asp
 995 1000 1005

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Gly Tyr Val Ser Lys Pro Phe Glu Ala Glu Gln Leu Tyr Arg Glu Val
 1010 1015 1020

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1030

1035

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Phe Trp Met Leu Cys Cys Trp Phe Val Ser Trp Phe Val Asp Asn Gly

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Ile Glu Asp Lys Ser Gly Leu Leu Val Gly Ser Val Gly Asp Leu Glu

35 40 45

Lys Thr Lys Met Thr Thr Leu Lys Lys Lys Asn Lys Met Trp Phe Trp

50 55 60

Asn Lys Ile Ser Ser Ser Gly Leu Lys Ile Pro Ser Phe Ser Tyr Gln

65 70 75 80

Phe Leu Gly Ser Val Lys Phe Asn Lys Ala Trp Trp Arg Lys Leu Val

85 90 95

Val Val Trp Val Val Phe Trp Val Leu Val Ser Ile Trp Thr Phe Trp

100 105 110

Tyr Phe Ser Ser Gln Ala Met Glu Lys Arg Lys Glu Thr Leu Ala Ser

115 120 125

Met Cys Asp Glu Arg Ala Arg Met Leu Gln Asp Gln Phe Asn Val Ser

130	135	140			
Met Asn His Val Gln Ala	Met Ser Ile Leu	Ile Ser Thr Phe His His			
145	150	155	160		
Gly Lys Ile Pro Ser Ala	Ile Asp Gln Arg Thr Phe Ser Glu Tyr Thr				
	165	170	175		
Asp Arg Thr Ser Phe Glu Arg Pro Leu Thr Ser Gly Val Ala Tyr Ala					
	180	185	190		
Met Arg Val Leu His Ser Glu Arg Glu Glu Phe Glu Arg Gln Gln Gly					
	195	200	205		
Trp Thr Ile Arg Lys Met Tyr Ser Leu Glu Gln Asn Pro Val His Lys					
	210	215	220		
Asp Asp Tyr Asp Leu Glu Ala Leu Glu Pro Ser Pro Val Gln Glu Glu					
225	230	235	240		
Tyr Ala Pro Val Ile Phe Ala Gln Asp Thr Val Ser His Val Val Ser					
	245	250	255		
Leu Asp Met Leu Ser Gly Lys Glu Asp Arg Glu Asn Val Leu Arg Ala					
	260	265	270		
Arg Ser Ser Gly Lys Gly Val Leu Thr Ala Pro Phe Pro Leu Ile Lys					
	275	280	285		
Thr Asn Arg Leu Gly Val Ile Leu Thr Phe Ala Val Tyr Lys Arg Asp					
	290	295	300		
Leu Pro Ser Asn Ala Thr Pro Lys Glu Arg Ile Glu Ala Thr Asn Gly					
305	310	315	320		
Tyr Leu Gly Gly Val Phe Asp Ile Glu Ser Leu Val Glu Asn Leu Leu					
	325	330	335		
Gln Gln Leu Ala Ser Lys Gln Thr Ile Leu Val Asn Val Tyr Asp Ile					

545		550		555		560									
Ile	Gly	Asp	Pro	Gly	Arg	Phe	Arg	Gln	Ile	Leu	Thr	Asn	Leu	Met	Gly
		565		570		575									
Asn	Ser	Ile	Lys	Phe	Thr	Glu	Lys	Gly	His	Ile	Phe	Val	Thr	Val	His
		580		585		590									
Leu	Val	Asp	Glu	Leu	Phe	Glu	Ser	Ile	Asp	Gly	Glu	Thr	Ala	Ser	Ser
		595		600		605									
Pro	Glu	Ser	Thr	Leu	Ser	Gly	Leu	Pro	Val	Ala	Asp	Arg	Gln	Arg	Ser
		610		615		620									
Trp	Glu	Asn	Phe	Lys	Ala	Phe	Ser	Ser	Asn	Gly	His	Arg	Ser	Phe	Glu
625				630		635								640	
Pro	Ser	Pro	Pro	Asp	Ile	Asn	Leu	Ile	Val	Ser	Val	Glu	Asp	Thr	Gly
				645		650								655	
Val	Gly	Ile	Pro	Val	Glu	Ala	Gln	Ser	Arg	Ile	Phe	Thr	Pro	Phe	Met
				660		665								670	
Gln	Val	Gly	Pro	Ser	Ile	Ser	Arg	Thr	His	Gly	Gly	Thr	Gly	Ile	Gly
				675		680								685	
Leu	Ser	Ile	Ser	Lys	Cys	Leu	Val	Gly	Leu	Met	Lys	Gly	Glu	Ile	Gly
				690		695								700	
Phe	Ser	Ser	Thr	Pro	Lys	Val	Gly	Ser	Thr	Phe	Thr	Phe	Thr	Ala	Val
705				710		715								720	
Phe	Ser	Asn	Gly	Met	Gln	Pro	Ala	Glu	Arg	Lys	Asn	Asp	Asn	Asn	Gln
				725		730								735	
Pro	Ile	Phe	Ser	Glu	Phe	Arg	Gly	Met	Lys	Ala	Val	Val	Val	Asp	His
				740		745								750	
Arg	Pro	Ala	Arg	Ala	Lys	Val	Ser	Trp	Tyr	His	Phe	Gln	Arg	Leu	Gly

755	760	765
Ile Arg Val Glu Val Val Pro Arg Val Glu Gln Ala Leu His Tyr Leu		
770	775	780
Lys Ile Gly Thr Thr Thr Val Asn Met Ile Leu Ile Glu Gln Glu Ile		
785	790	795
Trp Asn Arg Glu Ala Asp Asp Phe Ile Lys Lys Leu Gln Lys Asp Pro		
805	810	815
Leu Phe Leu Ser Pro Lys Leu Ile Leu Leu Ala Asn Ser Val Glu Ser		
820	825	830
Ser Ile Ser Glu Ala Leu Cys Thr Gly Ile Asp Pro Pro Ile Val Ile		
835	840	845
Val Lys Pro Leu Arg Ala Ser Met Leu Ala Ala Thr Leu Gln Arg Gly		
850	855	860
Leu Gly Ile Gly Ile Arg Glu Pro Pro Gln His Lys Gly Pro Pro Ala		
865	870	875
Leu Ile Leu Arg Asn Leu Leu Leu Gly Arg Lys Ile Leu Ile Val Asp		
885	890	895
Asp Asn Asn Val Asn Leu Arg Val Ala Ala Gly Ala Leu Lys Lys Tyr		
900	905	910
Gly Ala Asp Val Val Cys Ala Glu Ser Gly Ile Lys Ala Ile Ser Leu		
915	920	925
Leu Lys Pro Pro His Glu Phe Asp Ala Cys Phe Met Asp Ile Gln Met		
930	935	940
Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Ile Arg Asp Met Glu		
945	950	955
Glu Glu Met Asn Lys Arg Ile Lys Asn Gly Glu Ala Leu Ile Val Glu		

aga att gaa att tct gat tcc gag tca cta gaa aac ttg aaa agc agc 96

Arg Ile Glu Ile Ser Asp Ser Glu Ser Leu Glu Asn Leu Lys Ser Ser

20

25

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gat ttt tat caa ctg ggt ggt ggt ggt gct ctg aat tcg tca gaa aag 144

Asp Phe Tyr Gln Leu Gly Gly Gly Gly Ala Leu Asn Ser Ser Glu Lys

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ccg aga aag atc gat ttt tgg cgt tcg ggg ttg atg ggt ttt gcg aag 192

Pro Arg Lys Ile Asp Phe Trp Arg Ser Gly Leu Met Gly Phe Ala Lys

50

55

60

atg cag cag cag caa cag ctt cag cat tca gtg gcg gtg aag atg aac 240

Met Gln Gln Gln Gln Gln Leu Gln His Ser Val Ala Val Lys Met Asn

65

70

75

80

aat aat aat aat aac gat cta atg ggt aat aaa aaa ggg tca act ttc 288

Asn Asn Asn Asn Asn Asp Leu Met Gly Asn Lys Lys Gly Ser Thr Phe

85

90

95

ata caa gaa cat cga gca ttg tta cca aaa gct ttg att ctg tgg atc 336

Ile Gln Glu His Arg Ala Leu Leu Pro Lys Ala Leu Ile Leu Trp Ile
100 105 110

atc att gtt ggg ttt ata agc agt ggg att tat cag tgg atg gat gat 384

Ile Ile Val Gly Phe Ile Ser Ser Gly Ile Tyr Gln Trp Met Asp Asp
115 120 125

gct aat aag att aga agg gaa gag gtt ttg gtc agc atg tgt gat caa 432

Ala Asn Lys Ile Arg Arg Glu Glu Val Leu Val Ser Met Cys Asp Gln
130 135 140

aga gct aga atg ttg cag gat caa ttt agt gtt agt gtt aat cat gtt 480

Arg Ala Arg Met Leu Gln Asp Gln Phe Ser Val Ser Val Asn His Val
145 150 155 160

cat gct ttg gct att ctc gtc tcc act ttt cat tac cac aag aac cct 528

His Ala Leu Ala Ile Leu Val Ser Thr Phe His Tyr His Lys Asn Pro
165 170 175

tct gca att gat cag gag aca ttt gcg gag tac acg gca aga aca gca 576

Ser Ala Ile Asp Gln Glu Thr Phe Ala Glu Tyr Thr Ala Arg Thr Ala

180

185

190

ttt gag aga ccg ttg cta agt gga gtg gct tat gct gaa aaa gtt gtg 624

Phe Glu Arg Pro Leu Leu Ser Gly Val Ala Tyr Ala Glu Lys Val Val

195

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aat ttt gag agg gag atg ttt gag cgg cag cac aat tgg gtt ata aag 672

Asn Phe Glu Arg Glu Met Phe Glu Arg Gln His Asn Trp Val Ile Lys

210

215

220

aca atg gat aga gga gag cct tca ccg gtt agg gat gag tat gct cct 720

Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro

225

230

235

240

gtt ata ttc tct caa gat agt gtc tct tac ctt gag tca ctc gat atg 768

Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met

245

250

255

atg tca ggc gag gag gat cgt gag aat att ttg cga gct aga gaa acc 816

Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr
260 265 270

gga aaa gct gtc ttg act agc cct ttt agg ttg ttg gaa act cac cat 864

Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His
275 280 285

ctc gga gtt gtg ttg aca ttc cct gtc tac aag tct tct ctt cct gaa 912

Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu
290 295 300

aat ccg act gtc gaa gag cgt att gca gcc act gca ggg tac ctt ggt 960

Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly
305 310 315 320

ggt gcg ttt gat gtg gag tct cta gtc gag aat tta ctt ggt cag ctt 1008

Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu
325 330 335

gct ggt aac caa gca ata gtt gtg cat gtg tat gat atc acc aat gca 1056

Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala

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tca gat cca ctt gtc atg tat ggt aat caa gat gaa gaa gcc gac aga 1104

Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg

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Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys

370

375

380

cat aag atg ata tgc agg tac cac caa aag gca cca ata cca ttg aat 1200

His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn

385

390

395

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gtg ctc aca act gtg cca ttg ttc ttt gcg att ggt ttc ttg gtg ggt 1248

Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly

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410

415

tat ata ctg tat ggt gca gct atg cac ata gta aaa gtc gaa gat gat 1296

Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp

420

425

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ttc cat gaa atg caa gag ctt aaa gtg cga gca gaa gct gct gat gtc 1344

Phe His Glu Met Gln Glu Leu Lys Val Arg Ala Glu Ala Ala Asp Val
435 440 445

gct aaa tcg cag ttt ctt gct acc gtg tct cac gag atc agg aca cca 1392

Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr Pro
450 455 460

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Met Asn Gly Ile Leu Gly Met Leu Ala Met Leu Leu Asp Thr Glu Leu
465 470 475 480

agc tcg aca cag aga gat tac gct caa acc gct caa gta tgt ggt aaa 1488

Ser Ser Thr Gln Arg Asp Tyr Ala Gln Thr Ala Gln Val Cys Gly Lys
485 490 495

gct ttg att gca ttg ata aat gag gtt ctt gat cgc gcc aag att gaa 1536

Ala Leu Ile Ala Leu Ile Asn Glu Val Leu Asp Arg Ala Lys Ile Glu
500 505 510

gct gga aag ctg gag ttg gaa tca gta cca ttt gat atc cgt tca ata 1584

Ala Gly Lys Leu Glu Leu Glu Ser Val Pro Phe Asp Ile Arg Ser Ile
515 520 525

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530 535 540

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Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn
565 570 575

tcg gtt aaa ttc aca gag aaa gga cat atc ttt gtt aaa gtc cat ctt 1776

Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu
580 585 590

gcg gaa caa tca aaa gat gaa tct gaa ccg aaa aat gca ttg aat ggt 1824

Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly

595

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gga gtg tct gaa gaa atg atc gtt gtt tcc aaa cag tca agt tac aac 1872

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aca ttg agc ggt tac gaa gct gct gat ggt cgg aat agc tgg gat tca 1920

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625

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Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile

645

650

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660

665

670

atc cct tta gtt gca caa ggc cgt gtg ttt atg ccg ttt atg caa gca 2064

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690 695 700

ata agc aag tgt ctt gtt gaa ctt atg cgt ggt cag ata aat ttc ata 2160

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705 710 715 720

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725 730 735

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Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val
740 745 750

gaa cac ttg cct tct act ttt aaa gga atg aaa gct ata gtt gtt gat 2304

Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp

755

760

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gct aag cct gtt aga gct gct gtg act aga tac cat atg aaa aga ctc 2352

Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu

770

775

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785

790

795

800

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810

815

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820

825

830

aat gac tca gag att cgt tta ttg aat tca aga acc aac gga aac gtt 2544

Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val

835

840

845

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His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn
850 855 860

tcg gag ttc gac aga gct aaa tcc gca gga ttt gca gat acg gta ata 2640

Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile
865 870 875 880

atg aaa ccg tta aga gca agc atg att ggg gcg tgt ctg caa caa gtt 2688

Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val
885 890 895

ctc gag ctg aga aaa aca aga caa caa cat cca gaa gga tca tca ccc 2736

Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro
900 905 910

gca act ctc aag agc ttg ctt aca ggg aag aag att ctt gtg gtt gat 2784

Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp
915 920 925

gat aat ata gtt aac agg aga gta gct gca gga gct ctc aag aaa ttt 2832

Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe

930

935

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Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu

945

950

955

960

ctt cag att cca cac act ttc gat gct tgc ttc atg gat att caa atg 2928

Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met

965

970

975

cca cag atg gac gga ttt gaa gca act cgt cag ata aga atg atg gag 2976

Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu

980

985

990

aag gaa gct aaa gag aag acg aat ctc gaa tgg cat tta ccg att cta 3024

Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu

995

1000

1005

gcg atg act gcg gat gtg ata cac gcg acc tac gag gaa tgt ctg aaa 3072

Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys

1010

1015

1020

agt ggg atg gat ggt tac gtc tcc aaa cct ttt gaa gaa gag aat ctc 3120

Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu

1025

1030

1035

1040

tat aaa tcc gtt gcc aaa tca ttc aaa cct aat cct atc tca cct tcg 3168

Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser

1045

1050

1055

tcg taa

3174

Ser

<210> 6

<211> 1057

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Asn Trp Ala Leu Asn Asn His Gln Glu Glu Glu Glu Glu Pro Arg

1	5	10	15												
Arg	Ile	Glu	Ile	Ser	Asp	Ser	Glu	Ser	Leu	Glu	Asn	Leu	Lys	Ser	Ser
	20		25		30										
Asp	Phe	Tyr	Gln	Leu	Gly	Gly	Gly	Gly	Ala	Leu	Asn	Ser	Ser	Glu	Lys
	35		40		45										
Pro	Arg	Lys	Ile	Asp	Phe	Trp	Arg	Ser	Gly	Leu	Met	Gly	Phe	Ala	Lys
	50		55		60										
Met	Gln	Gln	Gln	Gln	Gln	Leu	Gln	His	Ser	Val	Ala	Val	Lys	Met	Asn
65			70		75									80	
Asn	Asn	Asn	Asn	Asn	Asp	Leu	Met	Gly	Asn	Lys	Lys	Gly	Ser	Thr	Phe
			85		90									95	
Ile	Gln	Glu	His	Arg	Ala	Leu	Leu	Pro	Lys	Ala	Leu	Ile	Leu	Trp	Ile
	100		105		110										
Ile	Ile	Val	Gly	Phe	Ile	Ser	Ser	Gly	Ile	Tyr	Gln	Trp	Met	Asp	Asp
	115		120		125										
Ala	Asn	Lys	Ile	Arg	Arg	Glu	Glu	Val	Leu	Val	Ser	Met	Cys	Asp	Gln
	130		135		140										
Arg	Ala	Arg	Met	Leu	Gln	Asp	Gln	Phe	Ser	Val	Ser	Val	Asn	His	Val
145			150		155									160	
His	Ala	Leu	Ala	Ile	Leu	Val	Ser	Thr	Phe	His	Tyr	His	Lys	Asn	Pro
			165		170									175	
Ser	Ala	Ile	Asp	Gln	Glu	Thr	Phe	Ala	Glu	Tyr	Thr	Ala	Arg	Thr	Ala
	180		185		190										
Phe	Glu	Arg	Pro	Leu	Leu	Ser	Gly	Val	Ala	Tyr	Ala	Glu	Lys	Val	Val
	195		200		205										
Asn	Phe	Glu	Arg	Glu	Met	Phe	Glu	Arg	Gln	His	Asn	Trp	Val	Ile	Lys

210	215	220	
Thr Met Asp Arg Gly Glu Pro Ser Pro Val Arg Asp Glu Tyr Ala Pro			
225	230	235	240
Val Ile Phe Ser Gln Asp Ser Val Ser Tyr Leu Glu Ser Leu Asp Met			
	245	250	255
Met Ser Gly Glu Glu Asp Arg Glu Asn Ile Leu Arg Ala Arg Glu Thr			
	260	265	270
Gly Lys Ala Val Leu Thr Ser Pro Phe Arg Leu Leu Glu Thr His His			
	275	280	285
Leu Gly Val Val Leu Thr Phe Pro Val Tyr Lys Ser Ser Leu Pro Glu			
	290	295	300
Asn Pro Thr Val Glu Glu Arg Ile Ala Ala Thr Ala Gly Tyr Leu Gly			
305	310	315	320
Gly Ala Phe Asp Val Glu Ser Leu Val Glu Asn Leu Leu Gly Gln Leu			
	325	330	335
Ala Gly Asn Gln Ala Ile Val Val His Val Tyr Asp Ile Thr Asn Ala			
	340	345	350
Ser Asp Pro Leu Val Met Tyr Gly Asn Gln Asp Glu Glu Ala Asp Arg			
	355	360	365
Ser Leu Ser His Glu Ser Lys Leu Asp Phe Gly Asp Pro Phe Arg Lys			
	370	375	380
His Lys Met Ile Cys Arg Tyr His Gln Lys Ala Pro Ile Pro Leu Asn			
385	390	395	400
Val Leu Thr Thr Val Pro Leu Phe Phe Ala Ile Gly Phe Leu Val Gly			
	405	410	415
Tyr Ile Leu Tyr Gly Ala Ala Met His Ile Val Lys Val Glu Asp Asp			

420	425	430
Phe His Glu Met Gln Glu Leu Lys Val Arg Ala Glu Ala Ala Asp Val		
435	440	445
Ala Lys Ser Gln Phe Leu Ala Thr Val Ser His Glu Ile Arg Thr Pro		
450	455	460
Met Asn Gly Ile Leu Gly Met Leu Ala Met Leu Leu Asp Thr Glu Leu		
465	470	475
Ser Ser Thr Gln Arg Asp Tyr Ala Gln Thr Ala Gln Val Cys Gly Lys		
485	490	495
Ala Leu Ile Ala Leu Ile Asn Glu Val Leu Asp Arg Ala Lys Ile Glu		
500	505	510
Ala Gly Lys Leu Glu Leu Glu Ser Val Pro Phe Asp Ile Arg Ser Ile		
515	520	525
Leu Asp Asp Val Leu Ser Leu Phe Ser Glu Glu Ser Arg Asn Lys Gly		
530	535	540
Ile Glu Leu Ala Val Phe Val Ser Asp Lys Val Pro Glu Ile Val Lys		
545	550	555
Gly Asp Ser Gly Arg Phe Arg Gln Ile Ile Ile Asn Leu Val Gly Asn		
565	570	575
Ser Val Lys Phe Thr Glu Lys Gly His Ile Phe Val Lys Val His Leu		
580	585	590
Ala Glu Gln Ser Lys Asp Glu Ser Glu Pro Lys Asn Ala Leu Asn Gly		
595	600	605
Gly Val Ser Glu Glu Met Ile Val Val Ser Lys Gln Ser Ser Tyr Asn		
610	615	620
Thr Leu Ser Gly Tyr Glu Ala Ala Asp Gly Arg Asn Ser Trp Asp Ser		

625 630 635 640
 Phe Lys His Leu Val Ser Glu Glu Gln Ser Leu Ser Glu Phe Asp Ile
 645 650 655
 Ser Ser Asn Val Arg Leu Met Val Ser Ile Glu Asp Thr Gly Ile Gly
 660 665 670
 Ile Pro Leu Val Ala Gln Gly Arg Val Phe Met Pro Phe Met Gln Ala
 675 680 685
 Asp Ser Ser Thr Ser Arg Asn Tyr Gly Gly Thr Gly Ile Gly Leu Ser
 690 695 700
 Ile Ser Lys Cys Leu Val Glu Leu Met Arg Gly Gln Ile Asn Phe Ile
 705 710 715 720
 Ser Arg Pro His Ile Gly Ser Thr Phe Trp Phe Thr Ala Val Leu Glu
 725 730 735
 Lys Cys Asp Lys Cys Ser Ala Ile Asn His Met Lys Lys Pro Asn Val
 740 745 750
 Glu His Leu Pro Ser Thr Phe Lys Gly Met Lys Ala Ile Val Val Asp
 755 760 765
 Ala Lys Pro Val Arg Ala Ala Val Thr Arg Tyr His Met Lys Arg Leu
 770 775 780
 Gly Ile Asn Val Asp Val Val Thr Ser Leu Lys Thr Ala Val Val Ala
 785 790 795 800
 Ala Ala Ala Phe Glu Arg Asn Gly Ser Pro Leu Pro Thr Lys Pro Gln
 805 810 815
 Leu Asp Met Ile Leu Val Glu Lys Asp Ser Trp Ile Ser Thr Glu Asp
 820 825 830
 Asn Asp Ser Glu Ile Arg Leu Leu Asn Ser Arg Thr Asn Gly Asn Val

835	840	845
His His Lys Ser Pro Lys Leu Ala Leu Phe Ala Thr Asn Ile Thr Asn		
850	855	860
Ser Glu Phe Asp Arg Ala Lys Ser Ala Gly Phe Ala Asp Thr Val Ile		
865	870	875
Met Lys Pro Leu Arg Ala Ser Met Ile Gly Ala Cys Leu Gln Gln Val		880
	885	890
Leu Glu Leu Arg Lys Thr Arg Gln Gln His Pro Glu Gly Ser Ser Pro		895
	900	905
Ala Thr Leu Lys Ser Leu Leu Thr Gly Lys Lys Ile Leu Val Val Asp		910
	915	920
Asp Asn Ile Val Asn Arg Arg Val Ala Ala Gly Ala Leu Lys Lys Phe		925
	930	935
Gly Ala Glu Val Val Cys Ala Glu Ser Gly Gln Val Ala Leu Gly Leu		940
945	950	955
Leu Gln Ile Pro His Thr Phe Asp Ala Cys Phe Met Asp Ile Gln Met		960
	965	970
Pro Gln Met Asp Gly Phe Glu Ala Thr Arg Gln Ile Arg Met Met Glu		975
	980	985
Lys Glu Ala Lys Glu Lys Thr Asn Leu Glu Trp His Leu Pro Ile Leu		990
	995	1000
Ala Met Thr Ala Asp Val Ile His Ala Thr Tyr Glu Glu Cys Leu Lys		1005
	1010	1015
Ser Gly Met Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Asn Leu		1020
1025	1030	1035
Tyr Lys Ser Val Ala Lys Ser Phe Lys Pro Asn Pro Ile Ser Pro Ser		1040

1045

1050

1055

Ser

<210> 7

<211> 125

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 7

Glu Thr Ser Val Lys Ile Leu Val Val Glu Asp Asn His Val Asn Gln

1

5

10

15

Glu Val Ile Lys Arg Met Leu Asn Leu Glu Gly Ile Glu Asn Ile Glu

20

25

30

Leu Ala Cys Asp Gly Gln Glu Ala Phe Asp Lys Val Lys Glu Leu Thr

35

40

45

Ser Lys Gly Glu Asn Tyr Asn Met Ile Phe Met Asp Val Gln Met Pro

50

55

60

Lys Val Asp Gly Leu Leu Ser Thr Lys Met Ile Arg Arg Asp Leu Gly

65

70

75

80

Tyr Thr Ser Pro Ile Val Ala Leu Thr Ala Phe Ala Asp Asp Ser Asn
85 90 95

Ile Lys Glu Cys Leu Glu Ser Gly Met Asn Gly Phe Leu Ser Lys Pro
100 105 110

Ile Lys Arg Pro Lys Leu Lys Thr Ile Leu Thr Glu Phe
115 120 125

<210> 8

<211> 118

<212> PRT

<213> Escherichia coli

<400> 1

Asn Asp Asp Met Met Ile Leu Val Val Asp Asp His Pro Ile Asn Arg
1 5 10 15

Arg Leu Leu Ala Asp Gln Leu Gly Ser Leu Gly Tyr Gln Cys Lys Thr
20 25 30

Ala Asn Asp Gly Val Asp Ala Leu Asn Val Leu Ser Lys Asn His Ile
35 40 45

Asp Ile Val Leu Ser Asp Val Asn Met Pro Asn Met Asp Gly Tyr Arg

50

55

60

Leu Thr Gln Arg Ile Arg Gln Leu Gly Leu Thr Leu Pro Val Ile Gly

65

70

75

80

Val Thr Ala Asn Ala Leu Ala Glu Glu Lys Gln Arg Cys Leu Glu Ser

85

90

95

Gly Met Asp Ser Cys Leu Ser Lys Pro Val Thr Leu Asp Val Ile Lys

100

105

110

Gln Ser Leu Thr Leu Tyr

115

<210> 9

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for PCR

<400> 9

tccccgcgga aaatgttctt acggttaggt ag

32

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 10

tcggtcgact tatgattctg tatctgaagg cga

33

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 11

tcagatatga actgggcact caac

24

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 12

ctcaatgctt ttgttccttg actc

24

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for PCR

<400> 13

accatgaact gggcactcaa caatcatcaa g

31

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 14

ggattacgac gaaggtgaga taggattagg

30

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 15

gatcccagct agctagggcc ctaccgcggg ga

32

<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 16

tccccgcgga aaatgttctt acggttaggt ag

32

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 17

tcggtcgact tatgattctg tatctgaagg cga

33

<210> 18

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 18

ctagtcctccg cggtagggcc ctagctagct gg

32

<210> 19

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 19

tccccgcgga aaatgtctat aacttgtag c

31

<210> 20

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 20

ctagctagct taacaagggtt caaagaatct tgc

33

<210> 21

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 21

tccccgcgga aaatgaaagc acgaggtgag agg

33

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 22

ctagctagct taacaagggtt caaagaattt gc

32